

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Genentech, Inc.
 Klein, Robert D.
 Moore, Mark W.
 Rosenthal, Arnon
 Ryan, Anne M.

(ii) TITLE OF INVENTION: USES OF GDNF AND GDNF RECEPTOR

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
 (B) STREET: 460 Point San Bruno Blvd
 (C) CITY: South San Francisco
 (D) STATE: California
 (E) COUNTRY: USA
 (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/615902
 (B) FILING DATE: 14-MAR-96

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/618236
 (B) FILING DATE: 14-MAR-96

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Torchia, PhD., Timothy E.
 (B) REGISTRATION NUMBER: 36,700
 (C) REFERENCE/DOCKET NUMBER: P0996P1PCT

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-8674
 (B) TELEFAX: 415/952-9881
 (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2378 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTCTATCGAT TGAATTC CCC GGGGATCCTC TAGAGATCCC TCGACCTCGA 50
 CCCACGCGTC CGCCGGGCGG CGGCTTTGGA TTTTGGGGGG GCGGGGACCA 100
 GCTGCGCGGC GGCACC ATG TTC CTA GCC ACT CTG TAC TTC 140

		Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe	
		1				5				
5	GCG CTG CCA CTC CTG GAT TTG CTG ATG TCC GCC GAG GTG 179									
	Ala Leu Pro Leu Leu Asp Leu Leu Met Ser Ala Glu Val									
	10 15 20									
	AGT GGT GGA GAC CGT CTG GAC TGT GTG AAA GCC AGC GAT 218									
	Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala Ser Asp									
	25 30									
10	CAG TGC CTG AAG GAA CAG AGC TGC AGC ACC AAG TAC CGC 257									
	Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg									
	35 40 45									
	ACA CTA AGG CAG TGC GTG GCG GGC AAG GAA ACC AAC TTC 296									
	Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe									
	50 55 60									
15	AGC CTG ACA TCC GGC CTT GAG GCC AAG GAT GAG TGC CGT 335									
	Ser Leu Thr Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg									
	65 70									
	AGC GCC ATG GAG GCC TTG AAG CAG AAG TCT CTG TAC AAC 374									
	Ser Ala Met Glu Ala Leu Lys Gln Lys Ser Leu Tyr Asn									
	75 80 85									
20	TGC CGC TGC AAG CGG GGC ATG AAG AAA GAG AAG AAT TGT 413									
	Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Lys Asn Cys									
	90 95									
	CTG CGT ATC TAC TGG AGC ATG TAC CAG AGC CTG CAG GGA 452									
	Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly									
	100 105 110									
	AAT GAC CTC CTG GAA GAT TCC CCG TAT GAG CCG GTT AAC 491									
	Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn									
	115 120 125									
30	AGC AGG TTG TCA GAT ATA TTC CGG GCA GTC CCG TTC ATA 530									
	Ser Arg Leu Ser Asp Ile Phe Arg Ala Val Pro Phe Ile									
	130 135									
	TCA GAT GTT TTC CAG CAA GTG GAA CAC ATT TCC AAA GGG 569									
	Ser Asp Val Phe Gln Gln Val Glu His Ile Ser Lys Gly									
	140 145 150									
35	AAC AAC TGC CTG GAC GCA GCC AAG GCC TGC AAC CTG GAC 608									
	Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp									
	155 160									
	GAC ACC TGT AAG AAG TAC AGG TCG GCC TAC ATC ACC CCC 647									
	Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro									
	165 170 175									
40	TGC ACC ACC AGC ATG TCC AAC GAG GTC TGC AAC CGC CGT 686									
	Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg									
	180 185 190									
	AAG TGC CAC AAG GCC CTC AGG CAG TTC TTC GAC AAG GTT 725									
	Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val									
	195 200									
	CCG GCC AAG CAC AGC TAC GGG ATG CTC TTC TGC TCC TGC 764									
	Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys									
	205 210 215									

CGG GAC ATC GCC TGC ACC GAG CGG CGG CGA CAG ACT ATC 803
Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile
220 225

5 GTC CCC GTG TGC TCC TAT GAA GAA CGA GAG AGG CCC AAC 842
Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Arg Pro Asn
230 235 240

TGC CTG AGT CTG CAA GAC TCC TGC AAG ACC AAT TAT ATC 881
Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile
245 250 255

10 TGC AGA TCT CGC CTT GCA GAT TTT TTT ACC AAC TGC CAG 920
Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln
260 265

15 CCA GAG TCA AGG TCT GTC AGC AAC TGT CTT AAG GAG AAC 959
Pro Glu Ser Arg Ser Val Ser Asn Cys Leu Lys Glu Asn
270 275 280

TAC GCA GAC TGC CTC CTG GCC TAC TCG GGA CTG ATT GGC 998
Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly
285 290

20 ACA GTC ATG ACT CCC AAC TAC GTA GAC TCC AGC AGC CTC 1037
Thr Val Met Thr Pro Asn Tyr Val Asp Ser Ser Ser Leu
295 300 305

AGC GTG GCA CCA TGG TGT GAC TGC AGC AAC AGC GGC AAT 1076
Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
310 315 320

25 GAC CTG GAA GAC TGC TTG AAA TTT CTG AAT TTT TTT AAG 1115
Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys
325 330

GAC AAT ACT TGT CTC AAA AAT GCA ATT CAA GCC TTT GGC 1154
Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly
335 340 345

30 AAT GGC TCA GAT GTG ACC ATG TGG CAG CCA GCC CCT CCA 1193
Asn Gly Ser Asp Val Thr Met Trp Gln Pro Ala Pro Pro
350 355

35 GTC CAG ACC ACC ACT GCC ACC ACT ACC ACT GCC TTC CGG 1232
Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Phe Arg
360 365 370

GTC AAG AAC AAG CCT CTG GGG CCA GCA GGG TCT GAG AAT 1271
Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn
375 380 385

40 GAG ATC CCC ACA CAC GTT TTA CCA CCC TGT GCG AAT TTG 1310
Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
390 395

45 CAG GCT CAG AAG CTG AAA TCC AAT GTG TCG GGT AGC ACA 1349
Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr
400 405 410

CAC CTC TGT CTT TCT GAT AGT GAT TTC GGA AAG GAT GGT 1388
His Leu Cys Leu Ser Asp Ser Asp Phe Gly Lys Asp Gly
415 420

50 CTC GCT GGT GCC TCC AGC CAC ATA ACC ACA AAA TCA ATG 1427
Leu Ala Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met

425 430 435

GCT GCT CCT CCC AGC TGC AGT CTG AGC TCA CTG CCG GTG 1466
 Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu Pro Val
 440 445 450

5 CTG ATG CTC ACC GCC CTT GCT GCC CTG TTA TCT GTA TCG 1505
 Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser
 455 460

10 TTG GCA GAA ACG TCG TAGCTGCATC CGGGAAAACA GTATGAAAAG 1550
 Leu Ala Glu Thr Ser
 465 468

ACAAAAGAGA ACCAAGTATT CTGTCCCTGT CCTCTTGAT ATCTGAAAAT 1600

CCAGTTTTAA AAGCTCCGTT GAGAAGCAGT TTCACCCAAC TGGAACCTTT 1650

TCCTTGTTTT TAAGAAAGCT TGTGGCCCTC AGGGGCTTCT GTTGAAGAAC 1700

TGCTACAGGG CTAATCCAA ACCCATAAGG CTCTGGGGCG TGGTGCGGCT 1750

15 TAAGGGGACC ATTTGCACCA TGTAAGCAA GCTGGGCTTA TCATGTGTTT 1800

GATGGTGAGG ATGGTAGTGG TGATGATGAT GGTAATTTTA ACAGCTTGAA 1850

CCCTGTTCTC TCTACTGGTT AGGAACAGGA GATACTATTG ATAAAGATTC 1900

TTCCATGTCT TACTCAGCAG CATTGCCTTC TGAAGACAGG CCCGCAGCCT 1950

AGTGTGAATG ACAAGTGGAG GTTGGCCTCA AGAGTGGACT TGGCAGACTC 2000

20 TACCTTGTAG TAATGTTTAC CTTTCCGTGT ATGGTCTCCA CAGAGTGTTT 2050

ATGTATTTAC AGACTGTTCT GTGATCCCCC AACAACAACA ACCACAAATT 2100

CCTTGGTCAC CTCCAAATGT AACCGGTCCT TTAGCCCAGT AGAGGAGGGT 2150

GGGTGTGGCC CTGGCACAGC TCCCGGATTG TTGATGGGCA CTCTCCTGAG 2200

CTTTGCTTGA GTGAGAAGCT GAATGTAGCT GAAAATCAAC TCTTCTTACA 2250

25 CTTAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2300

AAAAAAAAAA AAAAGGTTTA GGGATAACAG GGTAATGCGG CCGCGTCGAC 2350

CTGCAGAAGC TTGGCCGCCA TGGCCCAA 2378

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Extracellular Domain
 (B) LOCATION: 25
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: Mature Protein N-terminal
 (B) LOCATION: 25-427
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: Potential Glycosylation Site
 (B) LOCATION: 349
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: Potential Glycosylation Site
 (B) LOCATION: 408
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: Potential Glycosylation Site
 (B) LOCATION: 61
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe	Ala	Leu	Pro	Leu	Leu	Asp	Leu	1	5	10	15
Leu	Met	Ser	Ala	Glu	Val	Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	20	25	30	
Lys	Ala	Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	35	40	45	
Tyr	Arg	Thr	Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	50	55	60	
Ser	Leu	Thr	Ser	Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	65	70	75	
Met	Glu	Ala	Leu	Lys	Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	80	85	90	
Arg	Gly	Met	Lys	Lys	Glu	Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	95	100	105	
Met	Tyr	Gln	Ser	Leu	Gln	Gly	Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	110	115	120	
Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu	Ser	Asp	Ile	Phe	Arg	Ala	Val	125	130	135	
Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln	Val	Glu	His	Ile	Ser	Lys	140	145	150	
Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn	Leu	Asp	Asp	155	160	165	
Thr	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	Pro	Cys	Thr	Thr	170	175	180	
Ser	Met	Ser	Asn	Glu	Val	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	185	190	195	
Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	Tyr	Gly	200	205	210	
Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	Arg	215	220	225	
Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Arg				

	230	235	240
	Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile		
	245	250	255
5	Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu		
	260	265	270
	Ser Arg Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys		
	275	280	285
	Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn		
	290	295	300
10	Tyr Val Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys		
	305	310	315
	Ser Asn Ser Gly Asn Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn		
	320	325	330
15	Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe		
	335	340	345
	Gly Asn Gly Ser Asp Val Thr Met Trp Gln Pro Ala Pro Pro Val		
	350	355	360
	Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Phe Arg Val Lys Asn		
	365	370	375
20	Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His		
	380	385	390
	Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser		
	395	400	405
25	Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser Asp Ser Asp Phe		
	410	415	420
	Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile Thr Thr Lys		
	425	430	435
	Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu Pro Val		
	440	445	450
30	Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu Ala		
	455	460	465
	Glu Thr Ser		
	468		

(2) INFORMATION FOR SEQ ID NO:3:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40 His Gln Asn Leu Ser Asp Gly Lys
 1 5 8

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids

(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

His Gln Asn Ile Ser Asp Gly Lys
1 5 8

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His Gln Ser Leu Gly Thr Gln
1 5 7

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Ile Ser Ser His Leu Gly Gln
1 5 8

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Lys Asn Ser Ser Met Ile Ser Asn Thr Pro
1 5 10 11

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 418 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGGCACTGA ATCTAGGAAG GAGCCCAGGA TGAGCGGCAG GTTGGGTCGG 50
AACTGAACCC CTAAAAACGG GTCCGCCTCC CGCCCTCGCG CCCGCTCGGA 100
GCTGAGTCCC TGGCGGCGGT GGGCGGCAGA GCAACGGGGA GTCTGCTCTC 150
ACCTTGGATG GAGCTTAACT TTGAGTGGCC AGAGGAGCGC AGTCGCCCCG 200
GGATCTCTGC ACGCTGAGCT CTCTCCGCGA GATCCGGTGG CGGCTTTGGA 250
TTTTGGGGGG GCGGGGACCA GCTGCGCGGT GGCACCATGT TCCTAGCCAC 300

TCTGTACTTC GTGCTGCCAC TCCTGGATTT GCTGATGTCG GCCGAGGTGA 350
 GTGGTGGGGA CCGCTGGAC TGTGTGAAAG CCAGTGATCA GTGCCTGAAG 400
 GAACAGAGCT GCAGCACC 418

(2) INFORMATION FOR SEQ ID NO:9:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCCGCAAGT GCCACAAAGC CCTCAGGCAG TTCTTCGACA AAGTTCCAGC 50
 CAAGCACAGC TACGGGATGC TCTTCTGCTC CTGCCGGGAC GTCGCCTGCA 100
 CCGAGAGGCG GCGACAGACT ATCGTCCCTG TGTGCTCCTA TGAAGAACGA 150
 GAGAGGCCCA ACTGCCTGAA TCTGCAAGAC TCCTGCAAGA CAAATTACAT 200
 15 CTGCAGATCT CGCCTTGACG ATTTTITTTAC CAACTGCCAG CCAGAGTCAA 250
 GGTCTGTCAG CAACTGTCTT AAGGAGAACT ACGCAGACTG CCTCCTGGCC 300
 TACTCGGGAC TGATTGGCAC AGTCATGACT CCTAACTACA TAGACTCCAG 350
 CAGCCTCAGT GTGGCGCCGT GGTGCGATTG CAGCAACAGT GGCAATGACC 400
 TGGAAGATTG CCTGAAGTTT CTGAATTTT TTAAGGACAA TACGTGTCTC 450
 20 AAAAAATGCAA TTCAAGCCTT TGGCAATGGC TCGGATGTGA CCATGTGGCA 500
 GCCAGCCCCC CCAGTCCAGA CCACCACTGC CACGACTACC ACTGCCTTCC 550
 GGATCAAGAA CAAGCCTCTA GGGCCAGCAG GCTCTGAGAA TGAGATTCCC 600
 ACACACGTTT TACCACCGTG TGCTAATTG CAGGCACAGA AGCTGAAATC 650
 CAATGTATCG GGCAGTACAC ATCTCTGTCT TTCTGATAAT GATTACGGAA 700
 25 AGGATGGTCT CGCTGGTGCC TCCAGCCACA TAACCACAAA ATCAATGGCT 750
 GCTCCTCCCA GCTGCGGTCT GAGCTCACTG CCGGTGATGG TGTTACCCGC 800
 TCTGGCTGCC CTGTTGTCTG TATCATTGGC AGAAACATCG 840

(2) INFORMATION FOR SEQ ID NO:10:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35 AGGGAATTTG GCCCTCGAGG AAGGAGATTC GGCACGAGGC CAAGAGCAAC 50
 CATTGCCTGG ATGCTGCCAA GGCCTGCAAC CTGAATGACA ACTGCAAGAA 100
 GCTGCGCTCC TCCTACATCT CCATCTGCAA CCGCGAGATC TCGCCACCG 150

AGCGCTGCAA CCGCCGCAAG TGCCACAAGG CCCTGCGCCA GTTCTTCGAC 200
 CGGGTGCCCA GCGAGTACAC CTACCGCATG CTCTTCTGCT CCTGCCAAGA 250
 TCAGGCGTGC GCTGAGCNCG CGGNCAAAAC CATCCTGCCC AGCTGCTCCT 300
 ATGAGGACAA GGAGAAGCCC AACTGCNTGG ACNTGCGTGG CGTGTGCCGG 350

5 A 351

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCAACCATTG CCTGGATGCT GCCAAGGCCT GCAACCTGAA TGACAACTGC 50
 AAGAAGCTGC GTCCTCCTA CATCTCCATC TGCAACCGCG AGATCTCGCC 100
 CACCGAGCGC TGCAACCGCC GCAAGTGCCA CAAGGCCCTG CGCCAGTTCT 150
 TCGACCGGGT GCCCAGCGAG TACACCTACC GCATGCTCTT CTGCTCCTGC 200
 CAAGACCAGG CGTGCCTGA GCGCGCGGGC AAAACCATCC TGCCAGCTG 250
 CTCCTATGAG GACAAGGAGA AGCCCAACTG CCTGGACCTG CGTGGCGTGT 300
 GCCGACTGA CCACCTGTGT CGGTCCCGGC TNGCCGACTT TCCATGCCAA 350
 TTTGTTCGAG CCTTCTACC AGACGGGTCA CCAGGCTGCC CTNGCGGACA 400
 ATTTACCAGG GCGTGTCTTG GGGTCTTNAT GTTGGCATGA TTGGGTTTGA 450
 CAT 453

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAACCATTG CCTGGATGCT GCCAAGGCCT GCAACCTGAA TGACAACTGC 50
 AAGAAGCTGC GTCCTCCTA CATCTCCATC TGCAACCGCG AGATCTCGCC 100
 CACCGAGCGC TGCAACCGCC GCAAGTGCCA CAAGGCCCTG CGCCAGTTCT 150
 TCGACCGGGT GCCCAGCGAG TACACCTACC GCATGCTCTT CTGCTCCTGC 200
 C 201